

008271-112800

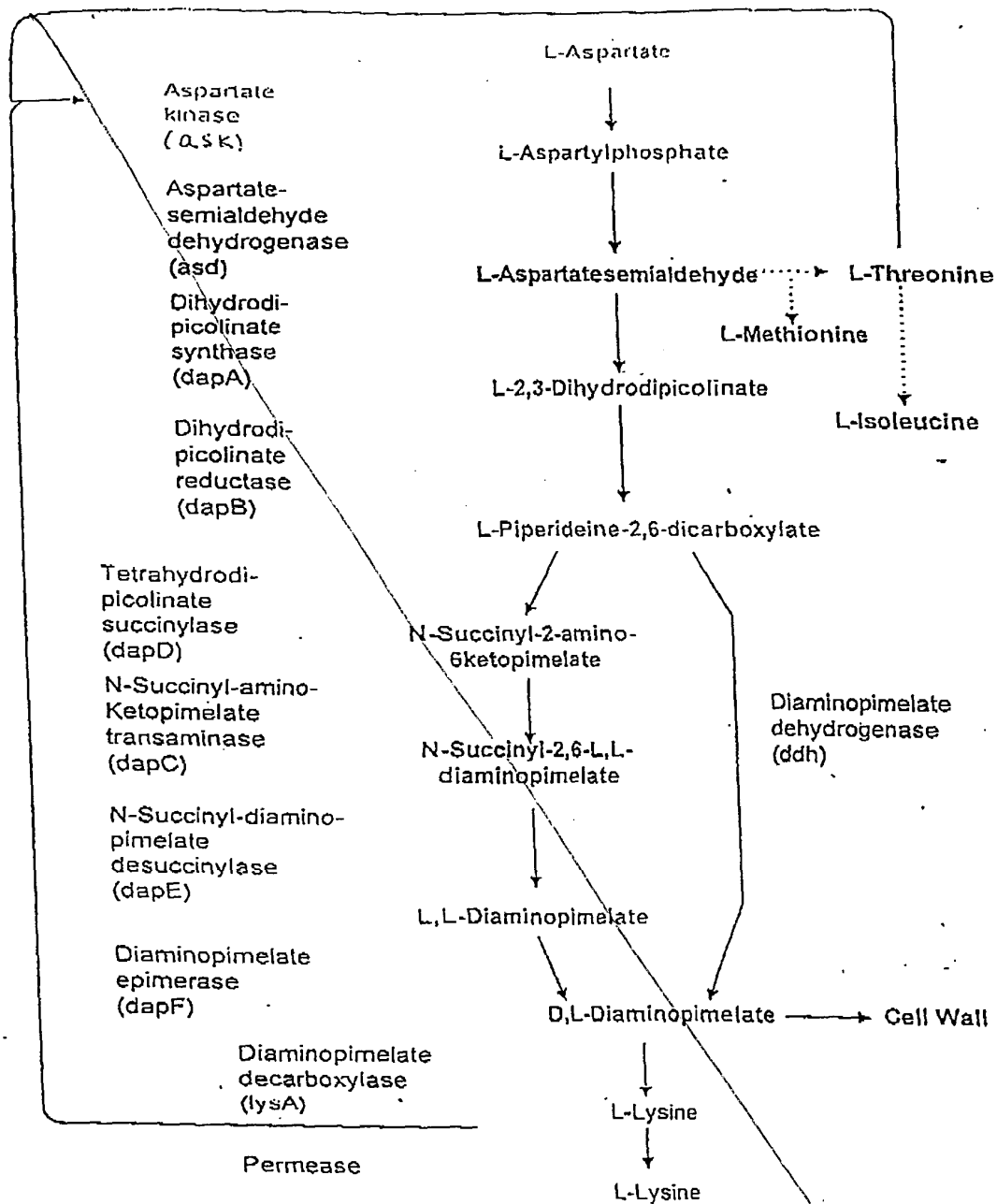


Figure 1

008211-14422650

Nucleotide sequence of ATCC21529 ask (SEQ ID NO:1)

```
1 GTGGCCCTGC TCGTACAGAA ATATGGCGGT TCCTCGCTTG AGAGTGC GGA
51 ACGCATTAGA AACGTCGCTG AACGGATCGT TGCCACCAAG AAGGCTGGAA
101 ATGATGTCGT GGTGTCTGC TCCGCAATGG GAGACACCAC GGATGAACCTT
151 CTAGAACTTG CAGCGGCAGT GAATCCCGTT CCGCCAGCTC GTGAAATGGA
201 TATGCTCCTG ACTGCTGGTG AGCGTATTTT TAACGCTCTC GTCGCCATGG
251 CTATTGAGTC CCTTGGCGCA GAAGCTCAAT CTTTCACTGG CTCTCAGGCT
301 GGTGTGCTCA CCACCGAGCG CCACGGAAAC GCACGCATTG TTGACGTCAC
351 ACCGGGTCGT GTGCGTGAAG CACTCGATGA GGGCAAGATC TGCATTGTTG
401 CTGGTTTTCA GGGTGTTAAT AAAGAAACCC GCGATGTCAC CACGTTGGGT
451 CGTGGTGGTT CTGACACCAC TGCAGTTGCG TTGGCAGCTG CTTTGAACGC
501 TGATGTGTGT GAGATTTACT CGGACGTTGA CGGTGTGTAT ACCGCTGACC
551 CGCGCATCGT TCCTAATGCA CAGAAGCTGG AAAAGCTCAG CTTCAAGAA
601 ATGCTGGAAC TTGCTGCTGT TGGCTCCAAG ATTTTGGTGC TCGCGAGTGT
651 TGAATACGCT CGTGCATTCA ATGTGCCACT TCGCGTACGC TCGTCTTATA
701 GTAATGATCC CGGCACTTTG ATTGCCGGCT CTATGGAGGA TATTCCTGTG
751 GAAGAAGCAG TCCTTACCGG TGTGCAACC GACAAGTCCG AAGCCAAAGT
801 AACC GTTCTG GGTATTTCCG ATAAGCCAGG CGAGGCTGCC AAGGTTTTCC
851 GTGCGTTGGC TGATGCAGAA ATCAACATTG ACATGGTTCT GCAGAACGTC
901 TCCTCTGTGG AAGACGGCAC CACCGACATC ACGTTCACCT GCCCTCGCGC
951 TGACGGACGC CGTGCGATGG AGATCTTGAA GAAGCTTCAG GTTCAGGGCA
1001 ACTGGACCAA TGTGCTTTAC GACGACCAGG TCGGCAAAGT CTCCCTCGTG
1051 GGTGCTGGCA TGAAGTCTCA CCCAGGTGTT ACCGCAGAGT TCATGGAAGC
1101 TCTGCGCGAT GTCAACGTGA ACATCGAATT GATTTCCATC TCTGAGATCC
1151 GCATTTCCGT GCTGATCCGT GAAGATGATC TGGATGCTGC TGCACGTGCA
1201 TTGCATGAGC AGTTCCAGCT GGGCGGCGAA GACGAAGCCG TCGTTTATGC
1251 AGGCACCGGA CGCTAA
```

Fig. 2

for amino acid sequence of ATCC 21529 anti:

[illegible]

Fig 3A

290x
114

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Fig. 38

3

Nucleotide. sequence of ATCC21529 asd (SEQ ID NO:2)

```

1   ATGACCACCA TCGCAGTTGT TGGTGAACC GGCCAGGTCG GCCAGGTTAT
51  GCGCACCTTT TTGGAAGAGC GCAATTCCC AGCTGACACT GTTCGTTTCT
101 TTGCTTCCCC GCGTTCCGCA GGCCGTAAGA TTGAATTCCG TGGCACGGAA
151 ATCGAGGTAG AAGACATTAC TCAGGCAACC GAGGAGTCCC TCAAGGGCAT
201 CGACGTTGCG TTGTTCTCTG CTGGAGGCAC CGCTTCCAAG CAGTACGCTC
251 CACTGTTTGC TGCTGCAGGC GCGACTGTTG TGGATAACTC TTCTGCTTGG
301 CGCAAGGACG ACGAGGTTCC ACTAATCGTC TCTGAGGTGA ACCCTTCCGA
351 CAAGGATTCCT CTGGTCAAGG GCATTATTGC GAATCCTAAC TGCACCACCA
401 TGGCTGCAAT GCCAGTGCTG AAGCCACTGC ACGATGCCGC TGGTCTTGTA
451 AAGCTTCACG TTTCTCTTA CCAGGCTGTT TCCGTTCTG GTCTTGACAGG
501 TGTGGAAACC TTGGCAAAGC AGGTTGCTGC AGTGGCGAC CACAACGTTG
551 AGTTCGTCCA TGATGGACAG GCTGCTGACC CAGGCGATGT CGGACCTTAC
601 GTTTCCCCAA TCGCTTACAA CGTGTGCCA TTCGCCGAA ACCTCGTCGA
651 TGACGGCACC TTCGAAACCG ACGAGAGCA GAAGCTGCGC AACGAATCCC
701 GCAAGATTCT CGGCCTCCA GACCTCAAGG TCTCAGGCAC CTGCGTCCGC
751 GTGCCGGTTT TCACCGGCCA CACGCTGACC ATTACGCGG AATTCGACAA
801 GGCAATCACC GTCGAGCAGG CGCAGGAGAT CTTGGGTGCC GCTTCAGGCG
851 TCGAGCTTGT CGACGTCCA ACCGACTTG CAGCTGCCGG CATGACGAA
901 TCCCTCGTTG GACGCATCCG TCAGSACTCC ACTGTCGACC ACAACCGCGG
951 TCTGGTTCTC GTCGTATCTG GCGATAACCT TCGCAAGGGC GCAGCACTGA
1001 ACACCATTCA GATTGCTGAG CTCCTGGTTA AGTAA

```

Fig. 4

SEQ. ID. No: 4 amino acid sequence of ATCC 21579 asd

```

ATGACCACCATCGCAGTTGTTGGTGCAATCCGGCCAGGTCCGGCCAGGTTATGCCGACGTTT
1 ----- 60
M T T I A V V G A T G Q V G Q V H R T F
TTGGAAGAGCGCAATTTCCGAGCTGACACTGTTGGTTCTTTGCTTCCCCCGGTTCCGCA
61 ----- 120
L E E R N F P A D T V R F F A S P R S A
GGCCGTAGATTGAATTCGGTGGCACGGAAATCGAGGTAGAAGACATTACTCAGGCAACC
121 ----- 180
G R K I E F R G T E I E V E D I T O A T
GAGGACTCCCTCAAGGGCATCGACGTTGGTTGTTCTCTGCTGGAGGCACCGCTTCCAAAG
181 ----- 240
E E S L K G I D V A L F S A G G T A S K
CAGTACGCTCCACTGTTTGGTGGCTGCAGGCGGAGCTGTTGGGATAACTCTTCTGTTGG
241 ----- 300
Q Y A P L F A A A G A T V V D N S S A W
CCCAACGACGACGAGGTTCCACTAATCGTCTGTGAGGTGAACCGTTCCGACAAAGATTCC
301 ----- 360
R K D D E V P L I V S E V N P S D K D S
CTGGTCAAGGGCATTATTGCCAATCCTAACTGCACCACCATGGCTGCAATGCCAGTGCTG
361 ----- 420
L V K G I I A N P R C T T H A A M P V L
AAGCCACTGCACGATGCCCGTGGTCTTTGTAAGGCTTCACGTTTCTCTTACCAGGCTGTT
421 ----- 480
K P L K D A A G L V L L H V S S Y Q A V
TCCCGTTCTGGTCTTGCAGGTGTGCAAACTTTGGCAAGCAGGTTGCTGCAGTTCCGCGAG
481 ----- 540
S G S G L A C V E T L A K Q V A A V G D
CACAACTGTGAGTTGCTCCATGATGGACAGGTTGCTGACGCAAGCGATGTCCGACCTTAC
541 ----- 600
K N V E F V H D G Q A A D A G D V G P Y
GTTTCCCAATCGCTTACAACGTGCTGCCATTCCCGGAAACCTCGTCCATGACGGGCACC
601 ----- 660
V S P I A Y H V L P F A C N L V D U G T
TTCGAAACCGACGAAGAGCAGAAGCTGCCAAGCAATCCCGAAGATTCTCGGCTCCCA
661 ----- 720
F E T D E E Q K L R K E S R K I L G L P
GACCTCAAGGTTCTCAGGCACCTCGGTCCGCTGCGGTTTTACCGGCCACACGCTGACC
721 ----- 780
D L K V S G T C V R V P V E T G H T L T
ATTACGCGCAATTTCGACAAAGCAATCACCCTCGACGAGCGGCGAGAGATCTTGGGTGCC
781 ----- 840
I H A E F D K A I T V E Q A Q E I L G A
GCTTCAGGCGTCGAGCTTGTCCAGCTCCCAACCCCACTTCCAGCTGCCCGCATTCAGCAA
841 ----- 900
A S G V E L V D V P T P L A A A C I O E

```

Fig 5A

SEQ ID NO:4
(Cont)

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901  TCCCTCGTTGGACGCATCCGTCAGGACTCCACTGTCGACGACAACCGCGGTCTGGTTCTC
-----+-----+-----+-----+-----+-----+-----+-----+ 960
      S L V G R I R Q D S T V D D N R G L V L
961  GTCGTATCTGGCGATAACCTTCGCAAGGGCGCAGCACTGAACACCATTTCAGATTGCTGAG
-----+-----+-----+-----+-----+-----+-----+-----+ 1020
      V V S G D N L R K G A A L N T I Q I A E
      CTGCTGGTTAAGTAA
1021 -----+----- 1035
      L L V K *

```

Fig 5B

09722441-112800

aa sequence
of dapt.

1. -

Fig 7

[illegible]

Nucleotide	sequence of	dapB (SEQ ID NO: 7)
1	ATGGGAATCA	AGGTTGGCGT TCTCCGAGCC AAGGSCCGTG TTGGTCAAAC
51	TATTGTGGCA	GCAGTCAATG AGTCCGACGA TCTGGAGCTT GTTGCAAGAG
101	TCGGCGTCGA	CGATGATTG AGCCTTCTGG TAGACAACGG CGCTGAAGTT
151	GTCGTTGACT	TCACCACTCC TAACGCTGTG ATGGGCAACC TGGAGTTCTG
201	CATCAACAAC	GGCATTCTG CGGTTGTTGG AACCACGGGC TTCGATAATG
251	CTCGTTTGGA	GCAGGTTGCG GcCTGGCTTG AAGGAAAAGA CAATGTCGGT
301	GTTCTGATCG	CACCTAACTT TGCTATCTCT GCGGTGTTGA CCATGGTCTT
351	TTCCAAGCAG	GCTGCCCGCT TCTTCGAATC AGCTGAAGTT ATTGAGCTGC
401	ACCACCCCAA	CAAGCTGGAT GCACCTTCAG GCACCGCGAT CCACACTGCT
451	CAGGGCATTG	CTGCCGCACG CAAAGAAGCA GGCATGGACG CACAGCCAGA
501	TGCGACCGAG	CAGGCACTTG AGGGTTCCCG TGGCGCAAGC GTAGATGGAA
551	TCCCAGTTCA	cGCAGTCCGC ATGTCCGGCA TGGTTGCTCA CGAGCAAGTT
601	ATCTTTGGCA	CCCAGGGTCA GACCTTGACC ATCAAGCAGG ACTCCTATGA
651	TCGCAACTCA	TTTGCACCAG GTGTCTTGGT GGGTGTGCGC AACATTGCAC
701	AGCACCCAGG	CCTAGTCGTA GGACTTGAGC ATTACCTAGG CCTGTAA

Fig 8

008277 " 142260

SEQID NO: 8 Amino acid sequence of dapB

```

1  ATGGGAATCAAGGTTGGCGTTCTCGGAGCCAAAGGCCGTGTTGGTCAAACCTATTGTGGCA
   -----+-----+-----+-----+-----+-----+-----+-----+ 60
   M G I K V G V L G A K G R V G Q T I V A
61  GCAGTCAATGAGTCCGACGATCTGGAGCTTGTTCGAGAGATCGGCGTCCGACGATGATTG
   -----+-----+-----+-----+-----+-----+-----+-----+ 120
   A V N E S D D L E L V A E I G V D D D L
121 AGCCTTCTGGTAGACAACGGCGCTGAAGTTGTCGTTGACTTCACCACTCCTAACGCTGTG
   -----+-----+-----+-----+-----+-----+-----+-----+ 180
   S L L V D N G A E V V V D F T T P N A V
181 ATGGGCAACCTGGAGTTCTGCATCAACAACGGCATTCTGCGGTTGTTGGAACACGGGC
   -----+-----+-----+-----+-----+-----+-----+-----+ 240
   M G N L E F C I N N G I S A V V G T T G
241 TTCGATaATGCTCGTTTGGAGCAGGTTCCGCGcCTGGCTTGAAGGAAAAGACAATGTCCGT
   -----+-----+-----+-----+-----+-----+-----+-----+ 300
   F D N A R L E Q V R A W L E G K D N V G
301 GTTCTGATCGCACCTAACTTTGCTATCTCTGCGGTGTTGACCATGGTCTTTTCCAAGCAG
   -----+-----+-----+-----+-----+-----+-----+-----+ 360
   V L I A P N F A I S A V L T M V F S K Q
361 GCTGCCCGCTTCTTCGAATCAGCTGAAGTTATTGAGCTGCACCACCCCAACAAGCTGGAT
   -----+-----+-----+-----+-----+-----+-----+-----+ 420
   A A R F F E S A E V I E L H H P N K L D
421 GCACCTTCAGGCACCGCGATCCACACTGCTCAGGGCATTGCTGCGGCACGCAAAGAAGCA
   -----+-----+-----+-----+-----+-----+-----+-----+ 480
   A P S G T A I H T A Q G I A A A R K E A
481 GGCATGGACGCACAGCCAGATGCGACCGAGCAGGCACTTGAGGGTTCCCGTGGCGCAAGC
   -----+-----+-----+-----+-----+-----+-----+-----+ 540
   G M D A Q P D A T E Q A L E G S R G A S
541 GTAGATGGAATCCCAGTTCAcGCAGTCCGCATGTCCGGCATGGTTGCTCAGCAGCAAGTT
   -----+-----+-----+-----+-----+-----+-----+-----+ 600
   V D G I P V H A V R M S G M V A H E Q V
601 ATCTTTGGCACCCAGGGTCAGACCTTGACCATCAAGCAGGACTCCTATGATCGCAACTCA
   -----+-----+-----+-----+-----+-----+-----+-----+ 660
   I F G T Q G Q T L T I K Q D S Y D R N S
661 TTGCAACCAGGTGTCTTGGTGGGTGTGCGCAACATTGCACAGCACCCAGGCCTAGTCGTA
   -----+-----+-----+-----+-----+-----+-----+-----+ 720
   F A P G V L V G V R N I A Q H P G L V V
721 GGACTTGAGCATTACCTAGGCCTGTAA
   -----+-----+-----+-----+-----+-----+-----+-----+ 747
   G L E H Y L G L +

```

Fig. 9

9

Nucleotide. sequence of *ddh* (SEQ ID NO: 1)

```

1   ATGCATTTCG GTAAGCTCGA CCAGGACAGT GCCACCACAA TTTTGGAGGA
51  TTACAAGAAC ATGACCAACA TCCGCGTAGC TATCGTgGGC TACGGAAACC
101 TGGGACGCAG CGTCGAAAAG CTTATTGCCA AGCAGCCCGA CATGGACCTT
151 GTAGGAATCT TCTCGCGCCG GGCCACCCTC GACACAAAGA CGCCAGTCTT
201 TGATGTCGCC GACGTGGACA AGCACGCCGA CGACGTGGAC GTGCTGTTCC
251 TGTGCATGGG CTCCGCCACC GACATCCCTG AGCAGGCACC AAAGTTCGCG
301 CAGTTCGCCT GCACCGTAGA CACCTACGAC AACCACCGCG ACATCCCACG
351 CCACCGCCAG GTCATGAACG AAGCCGCCAC CGCAGCCGGC AACGTTCGAC
401 TGGTCTCTAC CGGCTGGGAT CCAGGAATGT TCTCCATCAA CCGCGTCTAC
451 GCAGCGGCAG TCTTAGCCGA GCACCAGCAG CACACCTTCT GGGGCCCAGG
501 TTTGTCACAG GGCCACTCCG ATGCTTTGCG ACGCATCCCT GGC GTTCAA
551 AGGCcGTCCA GTACACCCTC CCATCCGAAG AaGCCCTGGA AAAGGCCCGC
601 CGTGGCGAAG CCGGCGACCT cACCGGAAG CAAACCCACA AGCGCCAATG
651 CTTTCGTGTT GCCGACGCGG CCGAcCACGA GCGCATCGAA AACGACATCC
701 GCACCATGCC TGATTA CTTC GTTGGCTACG AAGTCGAAGT CAACTTCATC
751 GACGAAGCAA CCTTgGACgC CGAGCACACC GGCATGCCAC ACGGcGGaCA
801 CGTGATcACC ACCGGCGACA CCGGTGGCTT CAACCACACC GTGGAATACA
851 TCCTgAAGCT GGACCGAAAC CCAGATTTCa CCGCTTCtTC ACAGATCGCT
901 TTCGGcCGCG CAGCTCACCG CATGAAGCAG CAGGGCCAAA GCGGtGCTTT
951 CACCGTCCTC GAAGTTGCTC CATActTGCT CTCCCCgGAG AACTTGGA tG
1001 ATCTGATCGC ACGCGACGTC TAA

```

Fig 10

SEQ ID 10: amino acid sequence of ddh.

SEQ ID
NO: 10

```

ATGTTATTTCTGTAAGCTCGACCAAGLHAGTGGCAAGCAATTTTGGAGATTACAAAGAC
60
M H F G F L D Q Q S A T T I L E D Y K N
ATGACCAACATCGGGTAGCTATCTTGGCTACGGAAAGCTGGGACCCAGCGTCGAAAG
120
H T N I F V A I V G Y C H I C R S V E K
CTTATTGCCAAGCAGCCGACATGGACCTTGTAGGAATCTTCTCGGGCCGGCCACCGTC
180
L I A K Q P D M D L V G I F S R R A T L
GACACAAAGACCCAGTCTTTGATGTGGCGGACCTGGACAAGCAGCCGACGCGTGGAG
240
D T K T E V F D V A D V D K H A D D V D
GTGCTCTTCTGTGATGGGCTCGCCACCCAGATCCCTGAGCAGGCACCAAGTTCCGG
300
V L F L C H G S A T O I P E Q A P K F A
CAGTTCGGCTGCAAGTAGACACCTACGACACCCAGCCGACATCCCAAGCCACCGCCAG
360
Q F A C T V D T Y D N H R D I P R H R Q
GTGATGAACGAAGCCGCCACCCAGCCGCAACGTTGCACTGGTCTCTACCGGCTGGAT
420
V M N E A A T A A C N V A L V S T G W D
CCAGGAATGTTCTCCATCAACCGGCTGTACGAGCGGCAGCTCTTAGCCGACACCCAGCAG
480
P G H F S I N R V Y A A A V L A E H O Q
CACACCTTCTGGGGCCAGGTTTGTACAGGGCCACTCCGATGCTTTGGAGGCATCCCT
540
H T F H G P G L S Q G H S D A L R P T P

GGCATTCAAAAGGCGCTCCAGTACACCTCCCATCCCAAGAGGCCCTGGCAAGCGCCCG
600
C V Q K A V Q Y T L P S E E A L E H A R
CGTGGGAAGCCGGCGAGCTACCGGAAAGCAAAACGACAAAGCCCAATGTTCTGTTGGT
660
R G E A G D L T G K Q T H K R O C F V V
GCCGACGGCGGGAACACGAGGCCATCGAAGGACATCCGACCATCCCTATTACTTC
720
A D A A D H E R I E N D I R T H F D Y F
GTTGGCTACGAAGTCGAAGTCAACTTCATCGACGAGCAACCTTGGACGCTGAGCAGACC
780
V G Y E V E V N F I D E A T L D A E H T
GGCATGCCACAGGGGGACAGTGATACCCACCGGGGACACCGGTGGCTTAACACACCC
840
G M P H G G H V I T T C D T G C F N H T
GTGGAAATACATCTGAAGCTGGACCGAAGCCAGATTTACCGCTTCTTACAGATCCCT
900
V E Y I L K L D R N P D F T A S S Q I A
TTGGGTCGGCGAGCTACCCCATCAAGCAGCAGGGCCAAAGCGGTGCTTACCGTCTCT

```

Fig 11A

003217-112244-00

SEQ ID NO:10
(cont)

```
901 ----- 960
      F G R A A H R M K Q Q G Q S G A F C Y L
      GAAGTIGCTCCATACCTGCTCTCCCCGGAAGAACTTGGATGATCTGATCGCACCGACGTC
961 ----- 1020
      E V A P Y L L S P E N L D D L I A P D V
      TAA
1021 --- 1023
```

Fig. 11B

008211-112800

Sequence of full length LysA from NRRL B-11474 (SEQ ID NO:
11); Underlined region: the priming site for lysA primer

ATGGCTACAGTTGAAAAATTTCAATGAACCTCCCGCACACGTATGGCCACGCAATGCAGTG
CGCCAAGAAGACGGCGTTGTACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA
TACGGAACCCCACTGTTGCTAGTCGACGAGGACGATTTCCGTTCCCGCTGTCCGACATG
GCTACCGCATTCGGTGGACCAAGCAATGTGCACTACGCATCCAAAGCGTTCTGACCAAG
ACCATTTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCGTCCATCAATGAA
CTGGGCATTCGCCCTGGCCGCTGGTTTCCCGGCCAGCCGTATCACCGCGCACGGCAACCAAC
AAAGGCGTAGAGTTCTGCCCGCGTTGGTTCAAAACGGTGTCCGGCATGTGGTGTGGAC
TCCGCGCAGGAATTGGAACTGCTGGATTACGTTGCCGCTGGTGAAGGCAAGATCCAGGAC
GTGTTGATCCCGCTGAAGCCAGGTATCGAAGCCACACCCACGATTCATCGCCACTAGC
CACGAAGACCAGAAGTTCCGATTCTCCCTGGCATCCGGTTCCGCATTCGAAGCAGCGAAA
GCAGCCAACTATGCAGAGAACTTGAACCTGGTTGGTCTGCACCTGCCATGTTGGTTCCAG
GTGTTTCGACGCCGAAGGCTTCAAGCTGGCAGCAGAGCGCGTGTGGGCTGTACTCAGAG
ATCCACAGCGAACTAGGTGTGCCCTTCCTGAGCTGGACCTCGGTGGCGGATACGGCATC
GCCTACACTGCAGATGAGGAACCACTCAACGTCGCAGAGTCCGCTCCGACCTACTCACC
GCAGTCGGAAAAATGGCAGCGGAACCTAGGCATCGACGCACCAACCGTGCTTGTGAGCCC
GGCCGCGCTATCCGAGGCCCCCTCCACCGTGACCATCTACGAAGTCGGCACCACCAAAAC
GTCCACGTAGACGACGACAAAACCCGCGCTACGTAGCCGTCGACGGAGGCATGTCCGAC
AACATCCGCCACGACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC
GAAGGAGACCCAGTAAGCACCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG
ATCAACGATGAAATCTACCCATCTGACATCACCAGCGCGGACTTCTCGCACTCGCAGCC
ACCGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCCTTCACACGGCCCCCGCTC
GTGTCGCTCCCGCTGGCAGCTCCCGCTCATGCTGGCGCGGAAACCCCTCGACGACATC
CTCTCACTAGAGGCATAA

Fig. 12

full length sequence of LysA (NRRL-B11474)
DIAMINOPIMELATE DECARBOXYLASE (Lys A) SEQ ID NO:12

MATVENFNELEPAHVWFRNAVVRQEDGVVTVAGVFLPDLAEEYGTPLFVVDEDDFRSRCDM
ATAFGGPGNVHYASKAFLTKTTARWVDEEGLALDIASINELGIALAAGFPASRITAHGNN
KGVFELRALVQNGVGHVVLDSAQELLLDYVAAGEGKIQDVLIRVKPGIEAETHEFLATS
HEDQKFGFSLASGSAFEAANAENLNVLGLHCHVGSQVFDACGFLAAERVVLGLYSQ
IHSELGVALPELDLGGGYGIAYTADDEFLNVAEVASDLLTAVGKMAELGIDAPTVLVEP
GRAIAGPSTVTIYEVGTTKNVHVDDDKTRRYVAVDGGMSDNIRPALYGYSEYDARVVSRFA
EGDPVSTRIVGSHCESGDILINDEIYPSDITSGDFLALAATGAYCYAMSSRYNAFTRPAV
VSVRAGSSRLMLRRETLDLILSLEA

Fig. 13

09722441.1.2300

Seq ID NO: 14 Full length amino acid sequence of LysA (pRSL)

```

ATGGCTACAGTTGAAAATTTCAATGAACITCCCGCACACGTATGGCCACGCCATGGCCGTG
1  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
M A T V E N F N E L P A H V W P R N A V
CGCCAAGAAGACGGCGTTGTCACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA
61  -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
R Q E D G V V T V A G V P L P D L A E E
TACGGAACCCCACTGTTCTAGTCGACGAGGACGATTCCCGTTCCTGTCGCGACATG
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
Y G T P L F V V D E D D F R S R C R D M
GCTACCGCATTCGGTGGACCAGGCAATGTGCACTACGCATCTAAAGCGTTCCTGACCAAG
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
A T A F G G P G N V H Y A S K A F L T K
ACCATTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCATCCATCAACGAA
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
T I A R W V D E E G L A L D I A S I N E
CTGGGCATTGCCCTGGCCGCTGGTTTCCCCGCCAGCCGTATCACCGCGCACGGCAACAAC
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
L G I A L A A G F P A S R I T A H G N N
AAAGGCGTAGAGTTCTCTGCGCGTGGTTCAAAACGGTGTGGGACACGTGGTGTCTGGAC
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
K G V E F L R A L V Q N G V G H V V L D
TCCGCACAGGAAGTAGAACTGTTGGATTACGTTGCCGCTGGTGAAGGCAAGATTTCAGGAC
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
S A Q E L E L L D Y V A A G E G K I Q D
GTGTTGATCCGCGTAAAGCCAGGCATCGAAGCACACACCCACGAGTTTCATCGCCACTAGC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
V L I R V K P G I E A H T H E F I A T S
CACGAAGACCAGAAGTTCCGATTCTCCCTGGCATCCGGTTCGCGATTCTGAAGCAGCAAAA
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
H E D Q K F G F S L A S G S A F E A A K
GCCGCCAACAACGCAGAAAACCTGAACCTGGTTGGCCTGCACTGCCACGTTGGTTCCCAG
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
A A N N A E N L N L V G L H C H V G S Q

```

Fig 15A

002244.1.12800

SEQ ID NO: 14 Lys A (pRS6)
(cont.)

```

661  GTGTTTCGACGCCGAAGGCTTCAAGCTGGCAGCAGAACGCGTGTGGGCCTGTACTCACAG 720
      -----+-----+-----+-----+-----+-----+-----+
      V F D A E G F K L A A E R V L G L Y S Q
      ATCCACACGCGAACTGGGCGTTGCCCTTCTGAACTGGATCTCGGTGGCGGATACGGCATT
721  -----+-----+-----+-----+-----+-----+-----+ 780
      I H S E L G V A L P E L D L G G G Y G I.
      GCCTATACCGCAGCTGAAGAACCCTCAACGTCGCAGAAGTTGCCTCCGACCTGCTCACC
781  -----+-----+-----+-----+-----+-----+-----+ 840
      A Y T A A E E F L N V A E V A S D L L T
      GCAGTCGGAAAAATGGCAGCGGAAGTGGCATCGACGCACCAACCGTGCTTGTGAGCCC
841  -----+-----+-----+-----+-----+-----+-----+ 900
      A V G K M A A E L G I D A R T V L V E P
      GGCCGCGCTATCGCAGGCCCTCCACCGTGACCATCTACGAAGTCGGCACCACCAAAGAC
901  -----+-----+-----+-----+-----+-----+-----+ 960
      G R A I A G P S T V T I Y E V G T T K D
      GTCCACGTAGACGACGACAAAACCCGCCGTTACATCGCCGTGGACGGAGGCATGTCCGAC
961  -----+-----+-----+-----+-----+-----+-----+ 1020
      V H V D D D K T R R Y I A V D G G M S D
      AACATCCGCCCAGCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
      N I R P A L Y G S E Y D A R V V S R F A
      GAAGGAGACCCAGTAAGCACCCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
      E G D P V S T R I V G S H C E S G D I L
      ATCAACGATGAATCTACCCATCTGACATCACCAGCGGCGACTTCCTTGCACTCGCAGCC
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
      I N D E I Y P S D I T S G D F L A L A A
      ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCTTCACACGGCCCGCCGTC
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
      T G A Y C Y A M S S R Y N A F T R P A V
      GTGTCCGTCCGCGCTGGCAGCTCCCGCTCATGCTGCGCCGCGAAACGCTCGACGACATC
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
      V S V R A G S S R L M L R R E T L D D I

```

Fig 15B

09722441.11800

seq ID NO: 14 Lys A (PRS6)
(cont)
CTCTCACTAGAGGCATAA
1321 ----- 1338
L S L E A *

003216 644260

fig 15C

Nucleotide. sequence of orf2 in dapBA operon SEQ ID NO: 15

```

1 GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTTT
51 TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GGCGCGGAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAACTTT TGATAAGCCG
151 AACCCTCGAA CTGCTTCCAA TGCTGCGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCAA TGCCACGATG TATATCCGAG
251 GCATTTCTCG GTCCGCGACC CATGAATTGG TCCGACACCG CCATTTTTC
301 TTCTCTCAAC TGTCTCAGCG TTTCGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCCACT CTCATCGATG AAGATCCGCA GTTGCCTGAA CTTTTCATGC
401 ACGCCATGGA TGAGTCTCGG TTCGCTTTCA ATGAGCTGCT TAATGCGCTG
451 GAAGAAAAAC TTGGCGATGA ACCGAATGCA CTTTAAAGGA AAAAGCAGGC
501 TCGTCAAGCA GCTCGCGCTG TGCTGCCCAA CGCTACAGAG TCCAGAATCG
551 TGGTGTCTGG AACTTCCGC ACCTGGAGGC ATTTCATTGG CATGCGAGCC
601 AGTGAACATG CAGACGTCGA AATCCGCGAA GTACCGGTAG GATGTTTAA
651 AAAGCTGCAG GTAGCAGCGC CAACTGTTTT CGGTGATTTT GAGATTGAAA
701 CTTTGGCAGA CGGATCGCAA ATGGCAACAA GCCCGTATGT CATGGACTTT
751 TAA

```

Fig 1b

SEQ ID No: 16

ORF2 amino acid sequence

```

1  GTGGCCGAACAAGTTAAATTGAGCGTGCAGTTGATAGCGTGCAGTTCTTTTACTCCACCC 60
   M A E Q V K L S V E L I A C S S F T P
61  GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCGAGTTTGCGGGT 120
   A D V E W S T D V E G A E A L V E F A G
121 CGTGCCTGCTACGAACTTTTGATAAGCCGAACCTCGAACTGCTTCCAATGCTGCGTAT 180
   R A C Y E T F D K P N P R T A S N A A Y
181 CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG 240
   L R H I M E V G H T A L L E H A N A T M
241 TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTCC 300
   Y I R G I S R S A T H E L V R H R H F S
301 TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT 360
   F S Q L S Q R F V H S G E S E V V V P T
361 CTCATCGATGAAGATCCGCGAGTTGCGTGAACCTTTTCATGCACGCCATGGATGAGTCTCGG 420
   L I D E D P Q L R E L F M H A M D E S R
421 TTCGCTTTCAATGAGCTGCTTAATGCGCTGGAAGAAAACTTGGCGATGAACCGAATGCA 480
   F A F N E L L N A L E E K L G D E P N A
481 CTTTTAAGGAAAAGCAGGCTCGTCAAGCAGCTCGCGCTGTGCTGCCCAACGCTACAGAG 540
   L L R K K Q A R Q A A R A V L P N A T E
541 TCCAGAATCGTGGTGTCTGAAACTTCCGCACCTGGAGGCATTTTCATTGGCATGCGAGCC 600
   S R I V V S G N F R T W R H F I G M R A
601 AGTGAACATGCAGACGTCGAAATCCGCGAAGTAGCGGTAGGATGTTTAAGAAAGCTGCAG 660
   S E H A D V E I R E V A V G C L R K L Q
661 GTAGCAGCGCCAACTGTTTTCGGTGATTTTGAGATTGAACTTTGGCAGACGGATCGCAA 720
   V A A P T V F G D F E I E T L A D G S Q
721 ATGGCAACAAGCCCGTATGTCATGGACTTTTAA 753
   M A T S P Y V M D F

```

fig 17

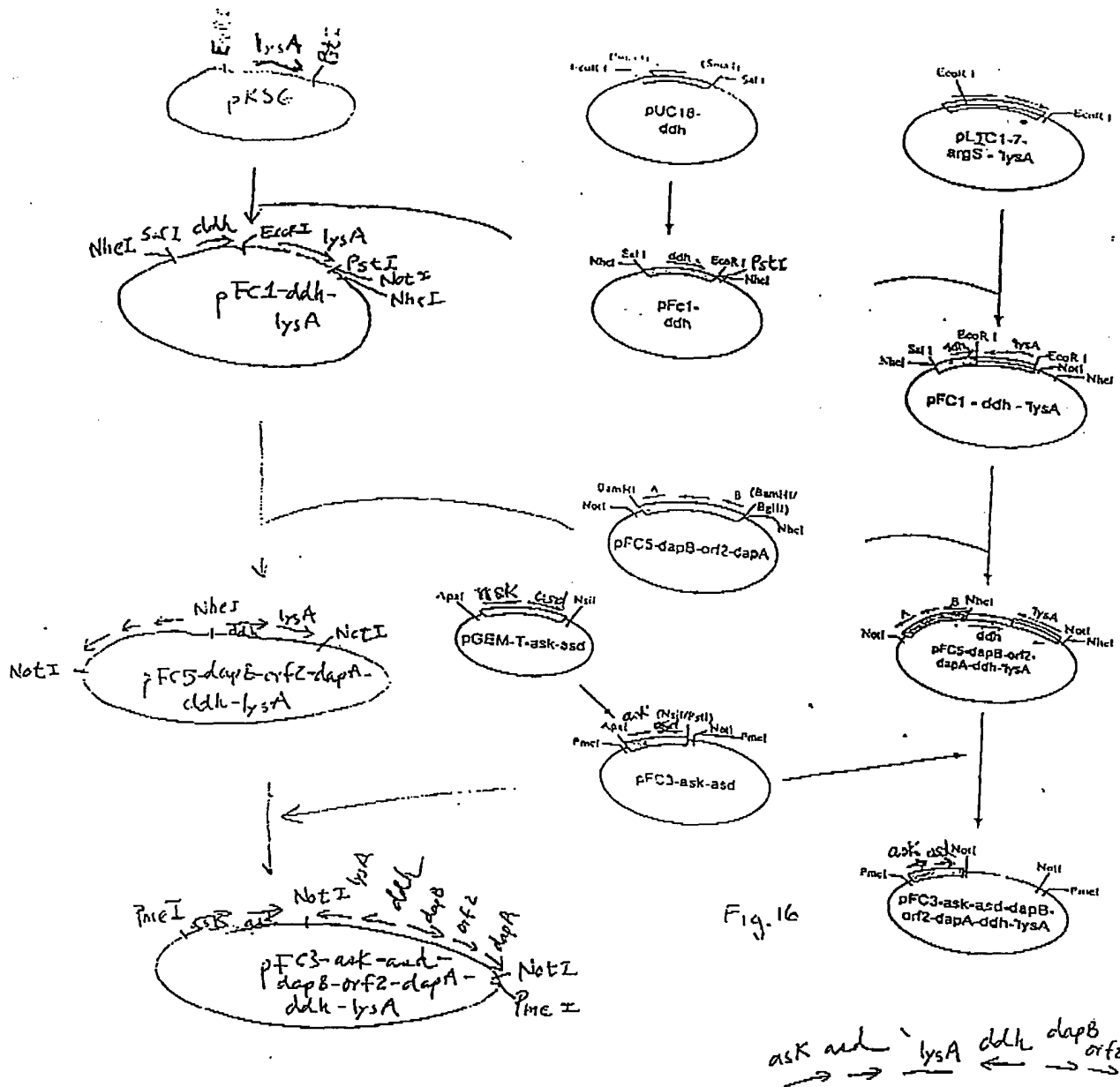


Fig. 18

ATCC 13032	1		50
N13			
ATCC 21529			
Consensus	HALVVQKYGG SSLESAERIR NVAERIVATK KAGNDVVVC SAMGDTTDEL		
	51		100
ATCC 13032			
N13			
ATCC 21529			
Consensus	LELAAAVNPV PPAREMDMLL TAGERISNAL VAMAIESLGA EAQSFQGSQA		
	101		150
ATCC 13032			
N13			
ATCC 21529			
Consensus	GVLTTTERHGN ARIVDVTPGR VREALDEGKI CIVAGFQGVN KETRDVTTLG		
	151		200
ATCC 13032			
N13			
ATCC 21529			
Consensus	RGGSDDTTAVA LAAALNADVC EIYSDVDGVY TADPRIVPNA QZLEKLSFEE		
	201		250
ATCC 13032			
N13			
ATCC 21529			
Consensus	MLELAAVGSK ILVLRSEYEA RAFNVPLRVR SSYSNDPQTL IAGSMEDIPV		
	251		300
ATCC 13032			
N13			
ATCC 21529			
Consensus	EEAVLTGVAT DKSEAKTVL GISDKPGEAA KVFRALADAE INIDMVLQNV		
	301		350
ATCC 13032		S	G
N13		A	D
ATCC 21529		A	G
Consensus	SSVEDGTTDI TFTCPRADGR RAKELKKLQ VQGNWTVLV DQVGEVSLV		
	351		400
ATCC 13032		T	
N13		T	
ATCC 21529		I	
Consensus	GAGNKSHPGV TAEFMEALRD VVNIELIST SEIRISVLIR EDDLDAARA		
	401	421	
ATCC 13032			
N13			
ATCC 21529			
Consensus	LHEQFQLGGE DEAVVYACTG R		

Fig. 19

Making pFC1-ddh-lysA

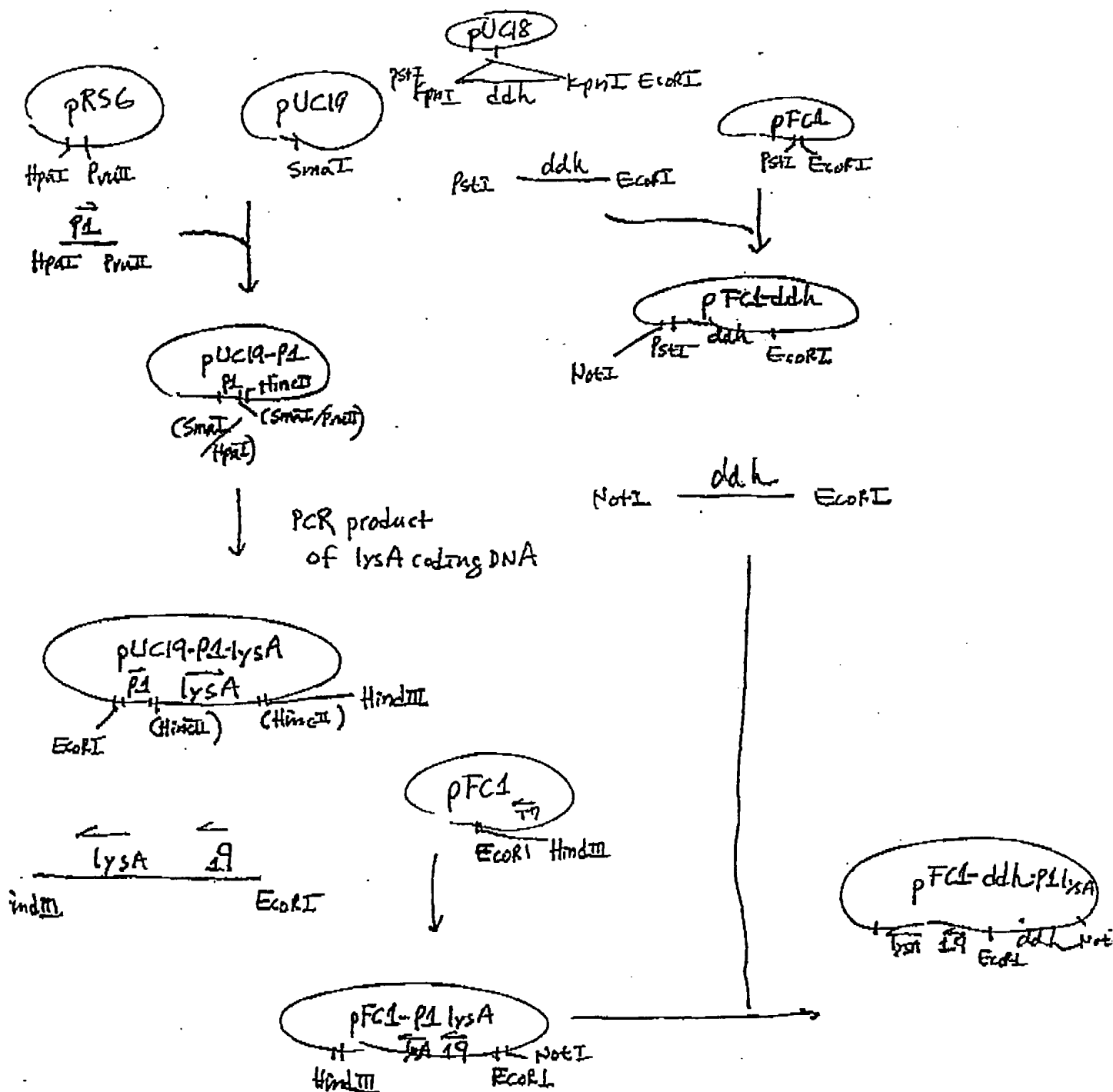


Fig. 21A

000211-112000

Making pDELia2-KDABHP1L

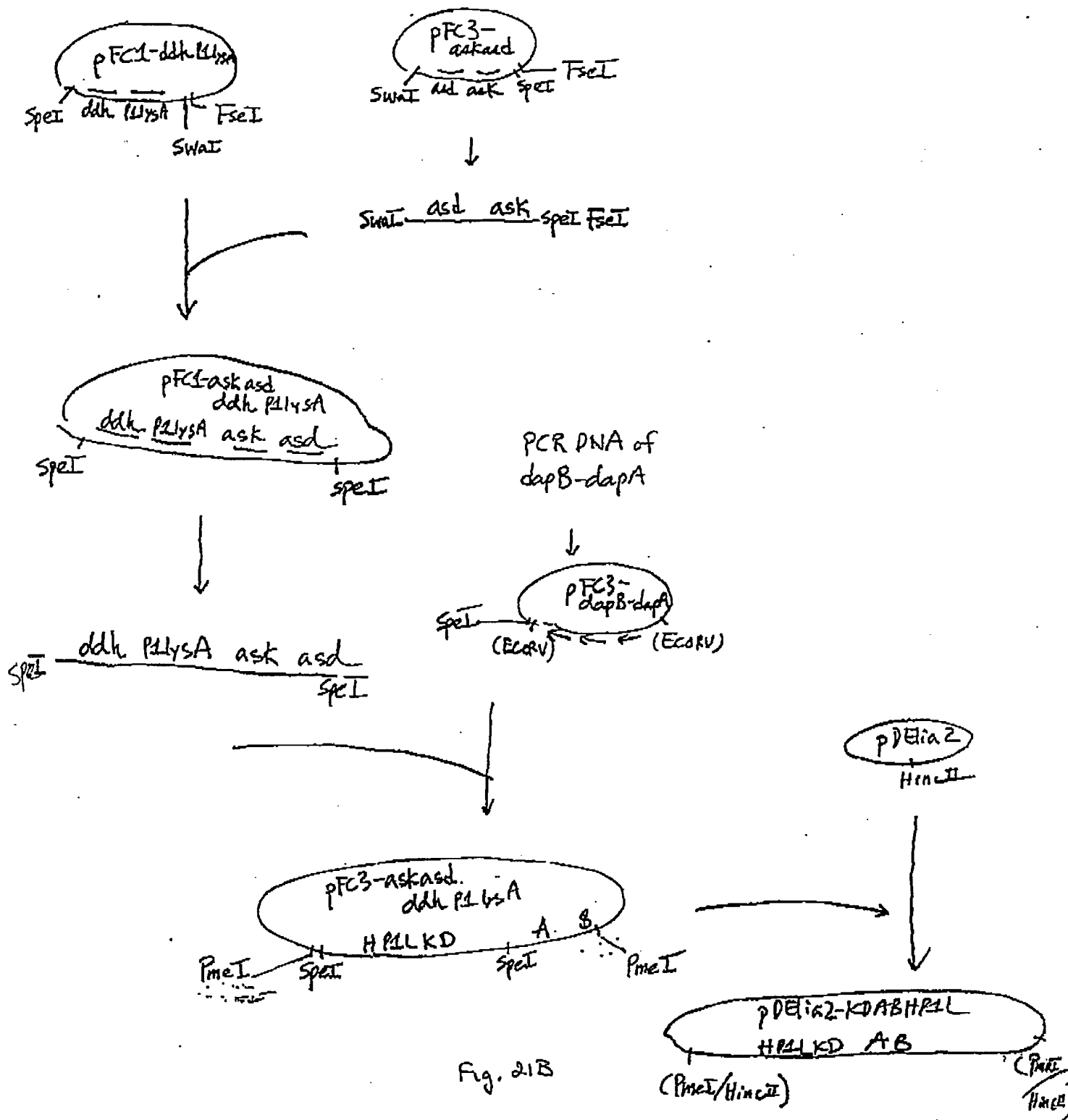
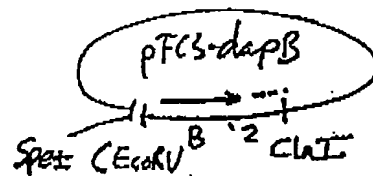
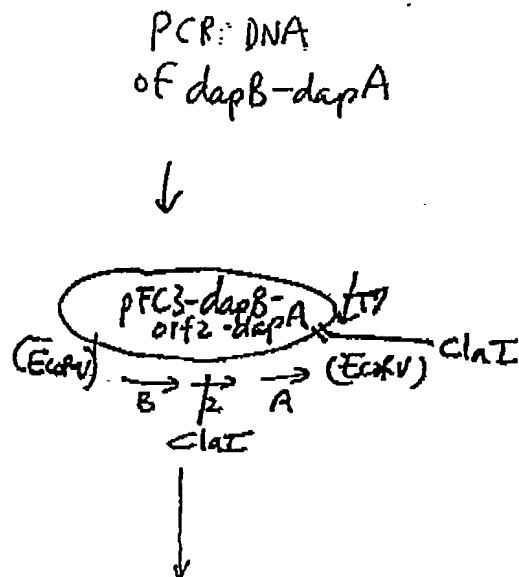
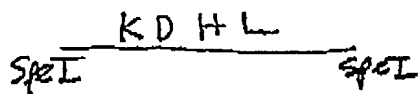
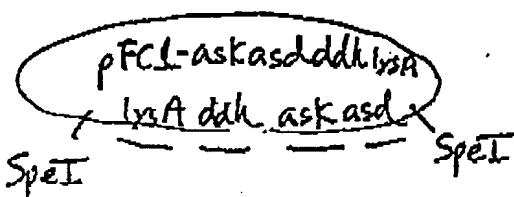
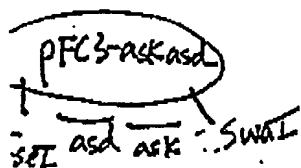
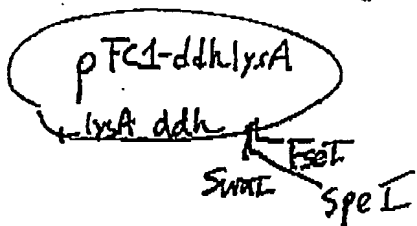


Fig. 21B

Making pDEla2Fc5-KDBHL

(from Fig 16)



(the truncated
orf 2 ----)

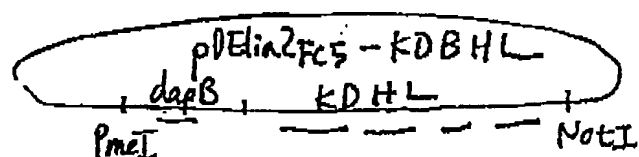
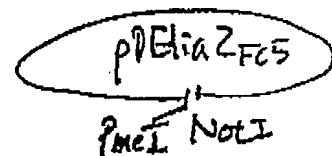
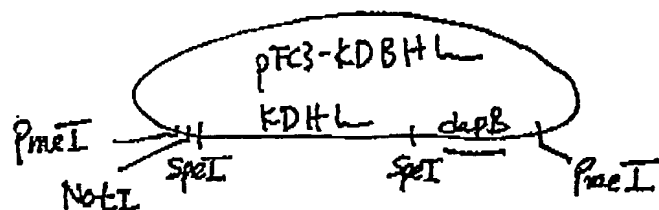


Fig. 22

orientation: $\leftarrow B \quad \leftarrow D \quad \leftarrow K \quad \leftarrow H \quad \leftarrow L$

008211-112800

nucleotide sequence of truncated ORF2

Seq ID NO: 18

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1  GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTTT
51  TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GGCGCGGAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAACTTT TGATAAGCCG
151 AACCCTCGAA CTGCTTCCAA TGCTGCGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCAA TGCCACGATG TATATCCGAG
251 GCATTTCTCG GTCGCGGACC CATGAATTGG TCCGACACCG CCATTTTTC
301 TTCTCTCAAC TGTCTCAGCG TTTCGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCACT CTCAT
```

Fig. 23

008277-112800

SEQ. ID. NO: 19

Truncated ORF2

amino acid sequence

1 GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC 60
 M A E Q V K L S V E L I A C S S F T P P
 61 GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCCGAGTTTSCGGGT 120
 A D V E W S T D V E G A E A L V E F A G
 121 CGTGCCTGCTACGAAACTTTTGATAAGCCGAACCCCTCGAACTGCTTCCAATGCTGCGTAT 180
 R A C Y E T F D K P N P R T A S N A A Y
 181 CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG 240
 L R H I M E V G H T A L L E H A N A T M
 241 TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTTC 300
 Y I R G I S R S A T H E L V R H R H F S
 301 TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGGCCACT 360
 F S Q L S Q R F V H S G E S E V V V P T
 361 CTCAT ...
 L (1)

fig. 24

003211-1422/60

Seq ID No: 20

Sequence of truncated Lys A (Lys A)

(NRRL-B11474)

ATGGCTACAGTTGAAAATTTCAATGAACTTCCCGCACACGTATGGCCACGCAATGCAGTG
CGCCAGAAGACGGCGTTGTACCGTCCGCTGGTGTGCCCTCTGCCCTGACCTCGCTGAAGAA
TACGGAACCCCACTGTTGCTAGTCCGACGAGGACGATTTCGGTTCCCGCTGTCCGACATG
GCTACCGCATTCGGTGGACCAAGCAATGTGCACTACGCATCCAAAGCGTTCCTGACCAAG
ACCATTCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCGTCCATCAATGAA
CTGGGCATTCGCTGGCCGCTGGTTTCCCGCCAGCCGTATCACCGCGCACGGCAACAC
AAAGGCGTAGAGTTCTCTGCGCGCGTTGGTTCAAAACGCTGTGCGGCATGTGGTGTCTGGAC
TCCGCGCAGGAATTGGAACCTGCTGGATTACGTTGCCGCTGGTGAAGGCAAGATCCAGGAC
GTGTTGATCCGCGTGAAGCCAGGTATCGAAGCCACACCCACGAGTTCATCGCCACTAGC
CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCCGCATTGAAGCAGCGAAA
GCAGCCAAACAATGCAGAGAACTTGAACCTGGTTGGTCTGCACTGCCATGTTGGTTCCAG
GTGTTGACGCCGAAGGCTTCAAGCTGGCAGCAGAGCCGCTGTTGGGCTGTACTCACAG
ATCCACAGCGAACTAGGTGTGCGCCCTTCTGAGCTGGACCTCGGTGGCGGATACGGCATC
GCCTACACTGCAGATGAGGAACCACTCAACGTCGCAGAAGTCGCCTCCGACCT

Fig. 25

Truncated sequence of LysA (NRRL-B11474).

DIAMINOPIMELATE DECARBOXYLASE (Lys A) SEQ ID NO: 21

MATVENFNELEPAHVWPRNAVVRQEDGVVTVAGVPLDAAEYGTPLFVVDDEDDFRSRCRM
ATAFGGGPGNVHYASKAFLTKTIARWVDEEGLALDIASINELGIALAAGFEASRITAHGNN
KGVFEFLRALVQNGVGHVVLDSAQEELLELDYVAAGEGKIQDVLRVKPGIEATHEFIATS
HEDQKFGFSLASGSFAFEAAKAANNAENLNVLGLHCHVGSQVFDAEGFKLAASRVLGLYSQ
IHSELGVALPELDLGGGYGIATYTADEEPIANVAEASDL

Fig. 26